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Spatial structure of oligopeptide PAP(248-261), the N-terminal fragment of the HIV enhancer prostatic acid phosphatase peptide PAP(248-286), in aqueous and SDS micelle solutions

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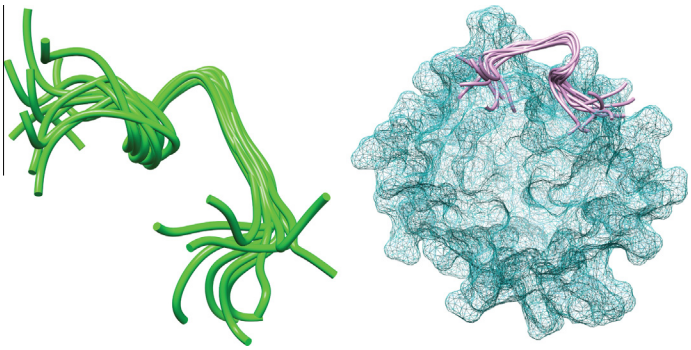
HIGHLIGHTS

- N-terminal fragment of the HIV enhancer prostatic acid phosphatase peptide PAP(248-286) was synthesized and characterized.
- Spatial structure of the peptide in water and in complex with sodium dodecyl sulfate was revealed.
- Complex formation was confirmed by ^{1}H NMR spectra.

GRAPHICAL ABSTRACT



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ABSTRACT

Prostatic acid phosphatase (PAP) is an enzyme that facilitates infection of cells by HIV. Its peptide fragment PAP(248-286) forms amyloid fibrils known as SEVI, which enhance attachment of the virus by viral adhesion to the host cell prior to receptor-specific binding via reducing the electrostatic repulsion between the membranes of the virus and the target cell. The secondary structure of PAP(248-286) in aqueous and SDS solutions can be divided into an N-terminal disordered region, an α-helical central part and an $\alpha/3_{10}$-helical C-terminal region (Nanga et al., 2009). In this work, we used NMR spectroscopy to study the spatial structure of the isolated N-terminal fragment of PAP(248-286), PAP(248-261) (GIHKQKEKSRLQGG), in aqueous and SDS micelle solutions. Formation of a PAP(248-261)-SDS complex was confirmed by chemical shift alterations in the ^{1}H NMR spectra of the peptide, as well as by the signs and values of Nuclear Overhauser Effect (NOE). In addition, the PAP(248-261) peptide does not form any specified secondary structure in either aqueous or SDS solutions.

Introduction

HIV (human immunodeficiency virus) affects the human immune system, causing the host to become highly sensitive to opportunistic infections that lead to illness and finally death. In spite of active expansion and contagion of HIV infection, the virus

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